Philip E Johnson

List of Publications by Year
in descending order

55 papers	1,789 citations	304743 22 h-index	276875 41 g-index
55 all docs	55 docs citations	55 times ranked	1768 citing authors

#	Article	IF	Citations
1	DNA binding by the antimalarial compound artemisinin. Scientific Reports, 2022, 12, 133.	3.3	6
2	How to Develop and Prove High-Efficiency Selection of Ligands from Oligonucleotide Libraries: A Universal Framework for Aptamers and DNA-Encoded Small-Molecule Ligands. Analytical Chemistry, 2021, 93, 5343-5354.	6.5	9
3	Visible Fluorescent Light-up Probe for DNA Three-Way Junctions Provides Hostâ€“Guest Biosensing Applications. ACS Applied Bio Materials, 2021, 4, 6732-6741.	4.6	8
4	Weak Binding of Levamisole by the Cocaine-Binding Aptamer Does Not Interfere with an Aptamer-Based Detection Assay. ACS Omega, 2021, 6, 24209-24217.	3.5	2
5	A Unique Conformational Distortion Mechanism Drives Lipocalin 2 Binding to Bacterial Siderophores. ACS Chemical Biology, 2020, 15, 234-242.	3.4	12
6	Designed Alteration of Binding Affinity in Structure-Switching Aptamers through the Use of Dangling Nucleotides. Biochemistry, 2020, 59, 663-670.	2.5	8
7	HACS1 signaling adaptor protein recognizes a motif in the paired immunoglobulin receptor B cytoplasmic domain. Communications Biology, 2020, 3, 672.	4.4	3
8	Reduction in Dynamics of Base pair Opening upon Ligand Binding by the Cocaine-Binding Aptamer. Biophysical Journal, 2020, 119, 1147-1156.	0.5	8
9	Thermodynamic analysis of cooperative ligand binding by the ATP-binding DNA aptamer indicates a population-shift binding mechanism. Scientific Reports, 2020, 10, 18944.	3.3	25
10	Analysis of the role played by ligand-induced folding of the cocaine-binding aptamer in the photochrome aptamer switch assay. Talanta, 2020, 217, 121022.	5.5	9
11	A proof of concept application of aptachain: ligand-induced self-assembly of a DNA aptamer. RSC Advances, 2019, 9, 1690-1695.	3.6	12
12	Aptamer facilitated purification of functional proteins. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2018, 1073, 201-206.	2.3	20
13	Development of a thermal-stable structure-switching cocaine-binding aptamer. Biochimie, 2018, 145, 137-144.	2.6	16
14	Nanomolar binding affinity of quinine-based antimalarial compounds by the cocaine-binding aptamer. Bioorganic and Medicinal Chemistry, 2018, 26, 5427-5434.	3.0	18
15	Salt-mediated two-site ligand binding by the cocaine-binding aptamer. Nucleic Acids Research, 2017, 45, gkw1294.	14.5	35
16	Comparison of the free and ligand-bound imino hydrogen exchange rates for the cocaine-binding aptamer. Journal of Biomolecular NMR, 2017, 68, 33-39.	2.8	17
17	Analysis of the interaction between the cocaine-binding aptamer and its ligands using fluorescence spectroscopy. Canadian Journal of Chemistry, 2017, 95, 1253-1260.	1.1	27
18	Optimizing Stem Length To Improve Ligand Selectivity in a Structure-Switching Cocaine-Binding Aptamer. ACS Sensors, 2017, 2, 1539-1545.	7.8	33

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19	Measuring Biomolecular DSC Profiles with Thermolabile Ligands to Rapidly Characterize Folding and Binding Interactions. Journal of Visualized Experiments, 2017, , .	0.3	0
20	Colorimetric detection of catalase and catalase-positive bacteria (E. coli) using silver nanoprisms. Analytical Methods, 2016, 8, 6625-6630.	2.7	13
21	Rapid characterization of folding and binding interactions with thermolabile ligands by DSC. Chemical Communications, 2016, 52, 13471-13474.	4.1	13
22	Structureâ€“affinity relationship of the cocaine-binding aptamer with quinine derivatives. Bioorganic and Medicinal Chemistry, 2015, 23, 2593-2597.	3.0	42
23	Pre-equilibration kinetic size-exclusion chromatography with mass spectrometry detection (peKSEC-MS) for label-free solution-based kinetic analysis of proteinâ€“small molecule interactions. Analyst, The, 2015, 140, 990-994.	3.5	9
24	Kinetic Size-Exclusion Chromatography with Mass Spectrometry Detection: An Approach for Solution-Based Label-Free Kinetic Analysis of Proteinâ€“Small Molecule Interactions. Analytical Chemistry, 2014, 86, 10016-10020.	6.5	20
25	Quantitative affinity electrophoresis of RNAâ€“small molecule interactions by cross-linking the ligand to acrylamide. Analytical Biochemistry, 2013, 442, 231-236.	2.4	1
26	Quinine Binding by the Cocaine-Binding Aptamer. Thermodynamic and Hydrodynamic Analysis of High-Affinity Binding of an Off-Target Ligand. Biochemistry, 2013, 52, 8652-8662.	2.5	69
27	Label-Free Solution-Based Kinetic Study of Aptamerâ€“Small Molecule Interactions by Kinetic Capillary Electrophoresis with UV Detection Revealing How Kinetics Control Equilibrium. Analytical Chemistry, 2011, 83, 8387-8390.	6.5	46
28	Engineering a Structure Switching Mechanism into a Steroid-Binding Aptamer and Hydrodynamic Analysis of the Ligand Binding Mechanism. Biochemistry, 2011, 50, 9368-9376.	2.5	25
29	Kinetic Capillary Electrophoresis with Massâ€Spectrometry Detection (KCEâ€MS) Facilitates Labelâ€Free Solutionâ€Based Kinetic Analysis of Proteinâ€“Small Molecule Binding. ChemBioChem, 2011, 12, 2551-2554.	2.6	21
30	Identification of RNAâ€“ligand interactions by affinity electrophoresis. Analytical Biochemistry, 2011, 409, 54-58.	2.4	2
31	Finding the Path in an RNA Folding Landscape. Structure, 2010, 18, 1550-1551.	3.3	0
32	Thermodynamic and NMR analysis of inhibitor binding to dihydrofolate reductase. Bioorganic and Medicinal Chemistry, 2010, 18, 8485-8492.	3.0	5
33	Defining the secondary structural requirements of a cocaine-binding aptamer by a thermodynamic and mutation study. Biophysical Chemistry, 2010, 153, 9-16.	2.8	89
34	Defining a Stem Length-Dependent Binding Mechanism for the Cocaine-Binding Aptamer. A Combined NMR and Calorimetry Study. Biochemistry, 2010, 49, 8478-8487.	2.5	85
35	Structure of the cytosineâ€“cytosine mismatch in the thymidylate synthase mRNA binding site and analysis of its interaction with the aminoglycoside paromomycin. Rna, 2009, 15, 911-922.	3.5	17
36	Enhanced NMR signal detection of imino protons in RNA molecules containing 3â€² dangling nucleotides. Journal of Biomolecular NMR, 2008, 40, 183-188.	2.8	3

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37	The three-dimensional structure of the Moorella thermoacetica selenocysteine insertion sequence RNA hairpin and its interaction with the elongation factor SelB. Rna, 2007, 13, 1948-1956.	3.5	4
38	The NMR and X-ray Structures of the Saccharomyces cerevisiae Vts1 SAM Domain Define a Surface for the Recognition of RNA Hairpins. Journal of Molecular Biology, 2006, 356, 274-279.	4.2	19
39	RNA recognition by the Vts1p SAM domain. Nature Structural and Molecular Biology, 2006, 13, 177-178.	8.2	61
40	Identification of a Novel Non-Carbohydrate Molecule that Binds to the Ribosomal A-Site RNA.. ChemInform, 2005, 36, no.	0.0	0
41	Assembly PCR oligo maker: a tool for designing oligodeoxynucleotides for constructing long DNA molecules for RNA production. Nucleic Acids Research, 2005, 33, W521-W525.	14.5	69
42	Identification of a novel non-carbohydrate molecule that binds to the ribosomal A-site RNA. Bioorganic and Medicinal Chemistry Letters, 2004, 14, 5987-5990.	2.2	23
43	A Mechanism for Plus-Strand Transfer Enhancement by the HIV-1 Nucleocapsid Protein during Reverse Transcriptionâ€,â€¡. Biochemistry, 2000, 39, 9084-9091.	2.5	94
44	Binding Site Analysis of Cellulose Binding Domain CBDN1from Endoglucanse C ofCellulomonas fimiby Site-Directed Mutagenesisâ€. Biochemistry, 2000, 39, 8844-8852.	2.5	42
45	The NMR Structure of the Nucleocapsid Protein from the Mouse Mammary Tumor Virus Reveals Unusual Folding of the C-Terminal Zinc Knuckleâ€,â€¡. Biochemistry, 2000, 39, 1604-1612.	2.5	36
46	Structure and Binding Specificity of the Second N-Terminal Cellulose-Binding Domain from Cellulomonas fimi Endoglucanase C,. Biochemistry, 2000, 39, 2445-2458.	2.5	54
47	The cellulose-binding domains from Cellulomonas fimi Î²-1,4-glucanase CenC bind nitroxide spin-labeled cellooligosaccharides in multiple orientations. Journal of Molecular Biology, 1999, 287, 609-625.	4.2	49
48	Stability and Oligosaccharide Binding of the N1 Cellulose-Binding Domain ofCellulomonas fimiEndoglucanase CenCâ€. Biochemistry, 1998, 37, 3529-3537.	2.5	17
49	Calcium Binding by the N-Terminal Cellulose-Binding Domain fromCellulomonasfimiÎ²-1,4-Glucanase CenCâ€. Biochemistry, 1998, 37, 12772-12781.	2.5	20
50	Specific (15)N, NH correlations for residues in(15) N, (13)C and fractionally deuterated proteins that immediately follow methyl-containing amino acids. Journal of Biomolecular NMR, 1997, 10, 283-288.	2.8	11
51	Cellulose-binding Domains.. Annals of the New York Academy of Sciences, 1996, 799, 418-424.	3.8	12
52	Structure of the N-Terminal Cellulose-Binding Domain ofCellulomonas fimiCenC Determined by Nuclear Magnetic Resonance Spectroscopyâ€,â€¡. Biochemistry, 1996, 35, 14381-14394.	2.5	138
53	The pKaof the General Acid/Base Carboxyl Group of a Glycosidase Cycles during Catalysis:Â A13C-NMR Study ofBacillus circulansXylanaseâ€. Biochemistry, 1996, 35, 9958-9966.	2.5	269
54	Interaction of Soluble Cellooligosaccharides with the N-Terminal Cellulose-Binding Domain ofCellulomonas fimiCenC. 2. NMR and Ultraviolet Absorption Spectroscopyâ€. Biochemistry, 1996, 35, 13895-13906.	2.5	88

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55	Probing the role of tryptophan residues in a celluloseâ€binding domain by chemical modification. Protein Science, 1996, 5, 2311-2318.	7.6	55